Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 10:33:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927027.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR927027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927027_1.fastq.gz SRR927027_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 10:33:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,385,318
Mapped reads	9,181,284 / 97.83%
Unmapped reads	204,034 / 2.17%
Mapped paired reads	9,181,284 / 97.83%
Mapped reads, first in pair	4,601,425 / 49.03%
Mapped reads, second in pair	4,579,859 / 48.8%
Mapped reads, both in pair	9,053,364 / 96.46%
Mapped reads, singletons	127,920 / 1.36%
Secondary alignments	0
Supplementary alignments	303,931 / 3.24%
Read min/max/mean length	30 / 101 / 102.35
Duplicated reads (estimated)	502,718 / 5.36%
Duplication rate	4.36%
Clipped reads	3,729,873 / 39.74%

2.2. ACGT Content

Number/percentage of A's	241,643,532 / 28.62%
Number/percentage of C's	165,987,206 / 19.66%
Number/percentage of T's	245,880,266 / 29.12%
Number/percentage of G's	190,748,792 / 22.59%
Number/percentage of N's	162,864 / 0.02%

GC Percentage	42.25%

2.3. Coverage

Mean	0.273
Standard Deviation	1.3673

2.4. Mapping Quality

Mean Mapping Quality	52.36

2.5. Insert size

Mean	350,574.94
Standard Deviation	5,780,473.85
P25/Median/P75	137 / 178 / 241

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	7,907,506
Insertions	146,934
Mapped reads with at least one insertion	1.57%
Deletions	439,084
Mapped reads with at least one deletion	4.66%
Homopolymer indels	51.75%

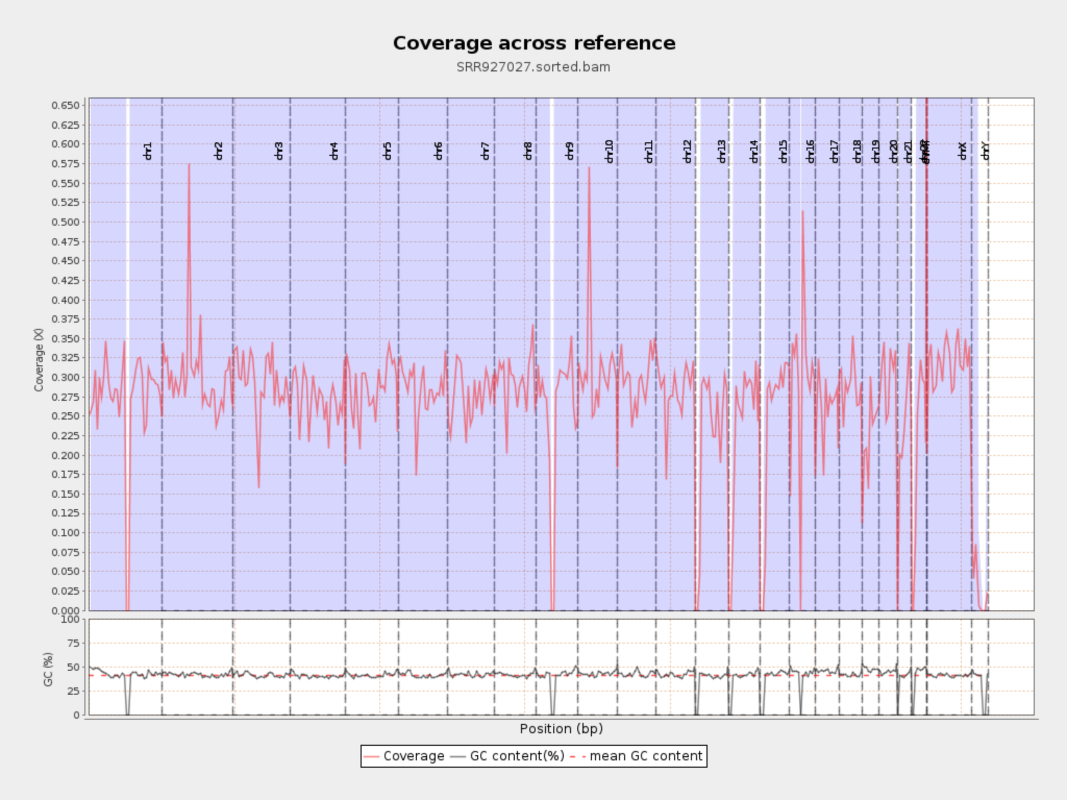
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

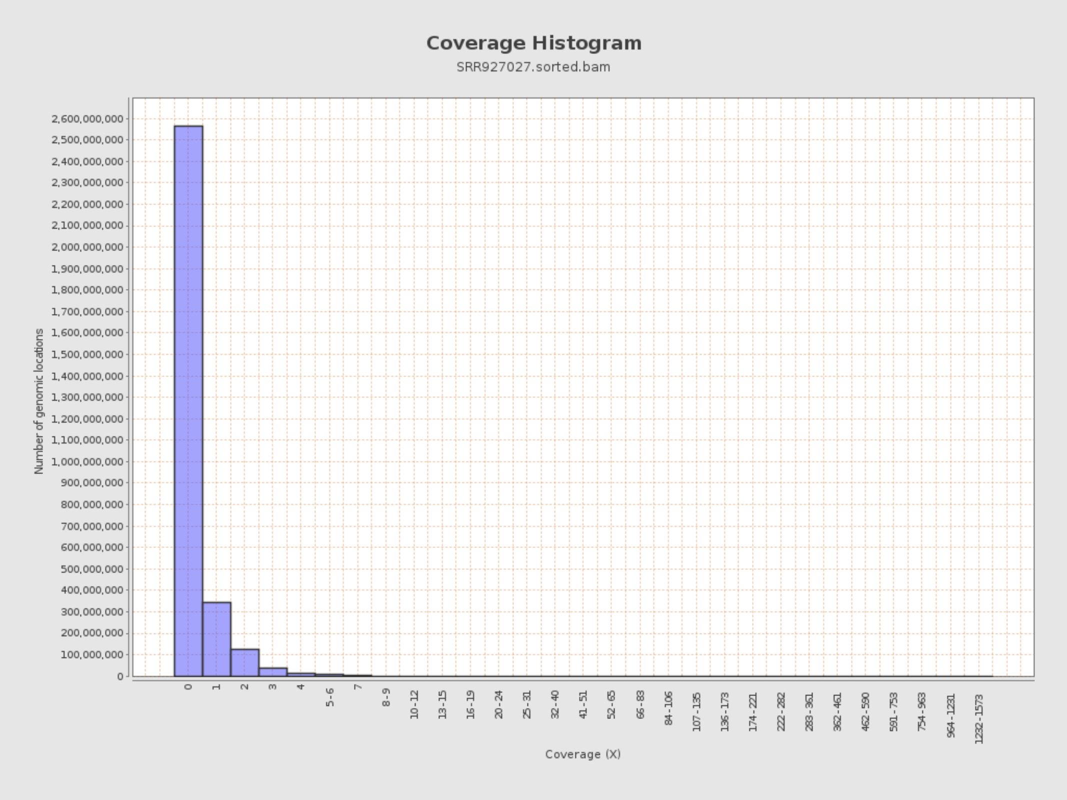
		bases	coverage	deviation
chr1	249250621	67303447	0.27	1.7918
chr2	243199373	73841267	0.3036	2.0712
chr3	198022430	58110662	0.2935	0.7659
chr4	191154276	51957410	0.2718	0.9667
chr5	180915260	51915899	0.287	0.7358
chr6	171115067	49022238	0.2865	0.8216
chr7	159138663	44138034	0.2774	1.0009
chr8	146364022	43494332	0.2972	0.8655
chr9	141213431	36046212	0.2553	1.5867
chr10	135534747	42292493	0.312	3.1231
chr11	135006516	39920993	0.2957	1.4741
chr12	133851895	37905395	0.2832	0.7435
chr13	115169878	25407987	0.2206	0.6418
chr14	107349540	24829413	0.2313	0.6746
chr15	102531392	24161249	0.2356	0.6787
chr16	90354753	26749594	0.2961	2.0343
chr17	81195210	21264368	0.2619	0.8122
chr18	78077248	22741922	0.2913	1.5932
chr19	59128983	13401876	0.2267	1.1651
chr20	63025520	18791430	0.2982	0.7921
chr21	48129895	10946424	0.2274	0.8734
chr22	51304566	10117518	0.1972	0.6486
chrMT	16571	19962	1.2046	1.631
chrX	155270560	49100258	0.3162	0.9005

chrY	59373566	1589568	0.0268	0.8488

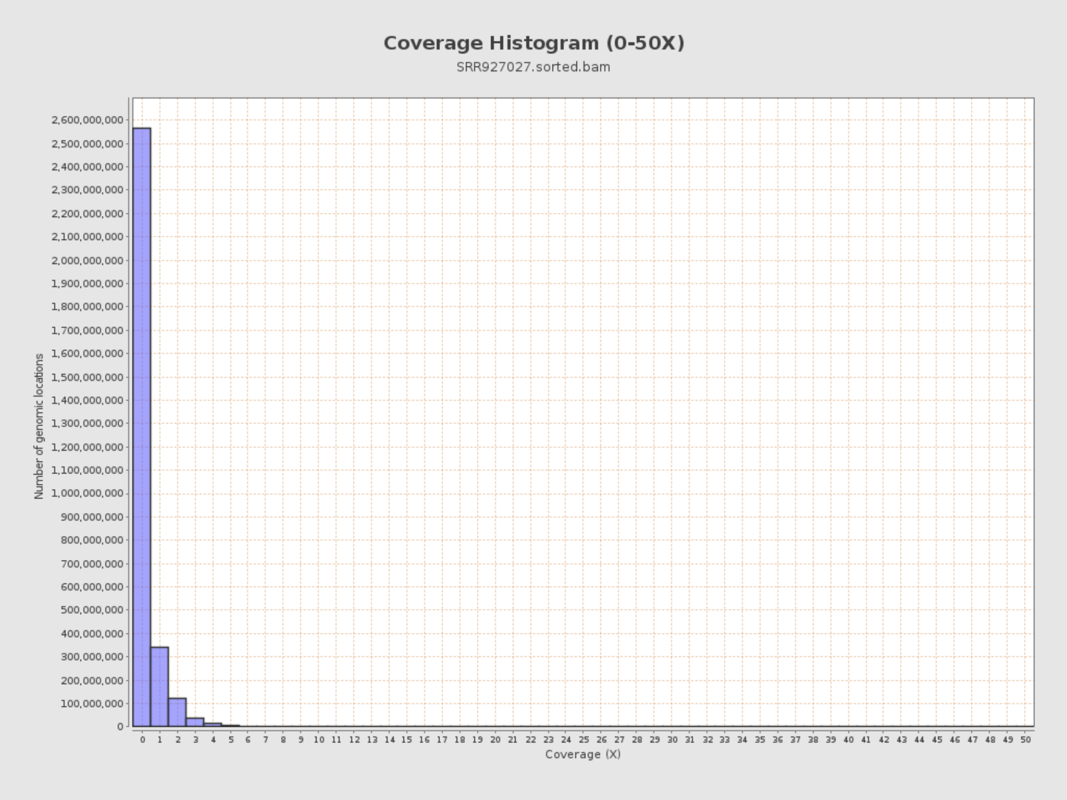
3. Results : Coverage across reference



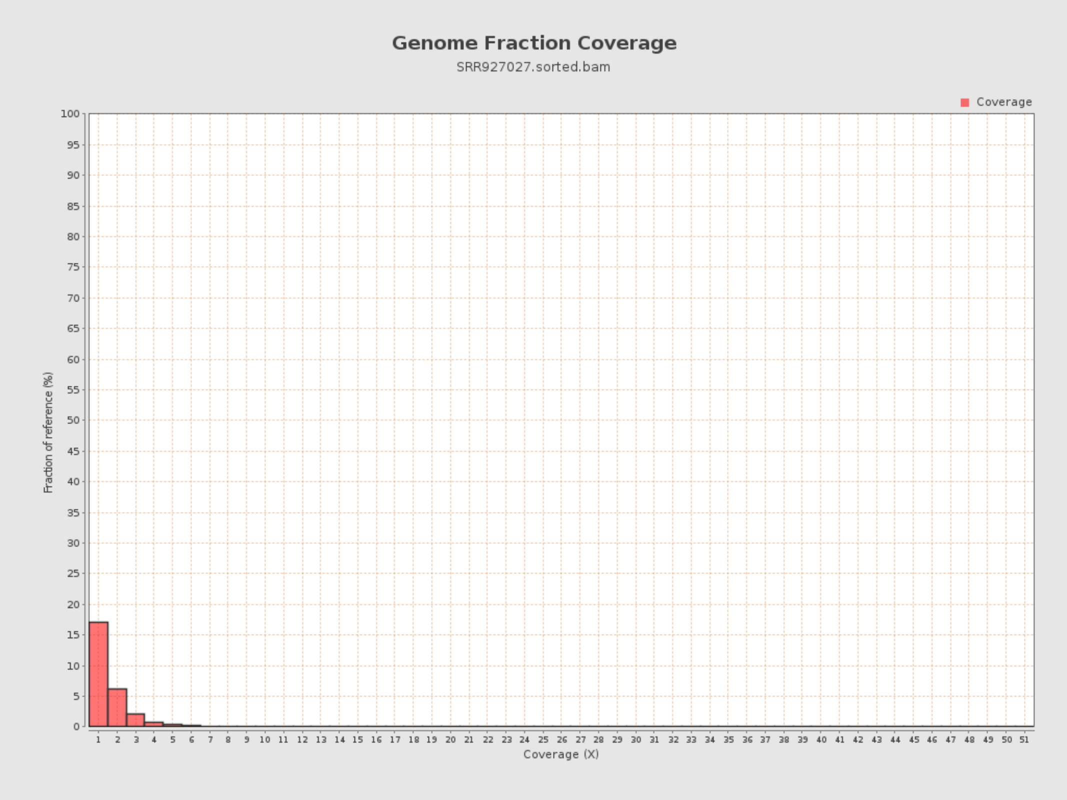
4. Results : Coverage Histogram



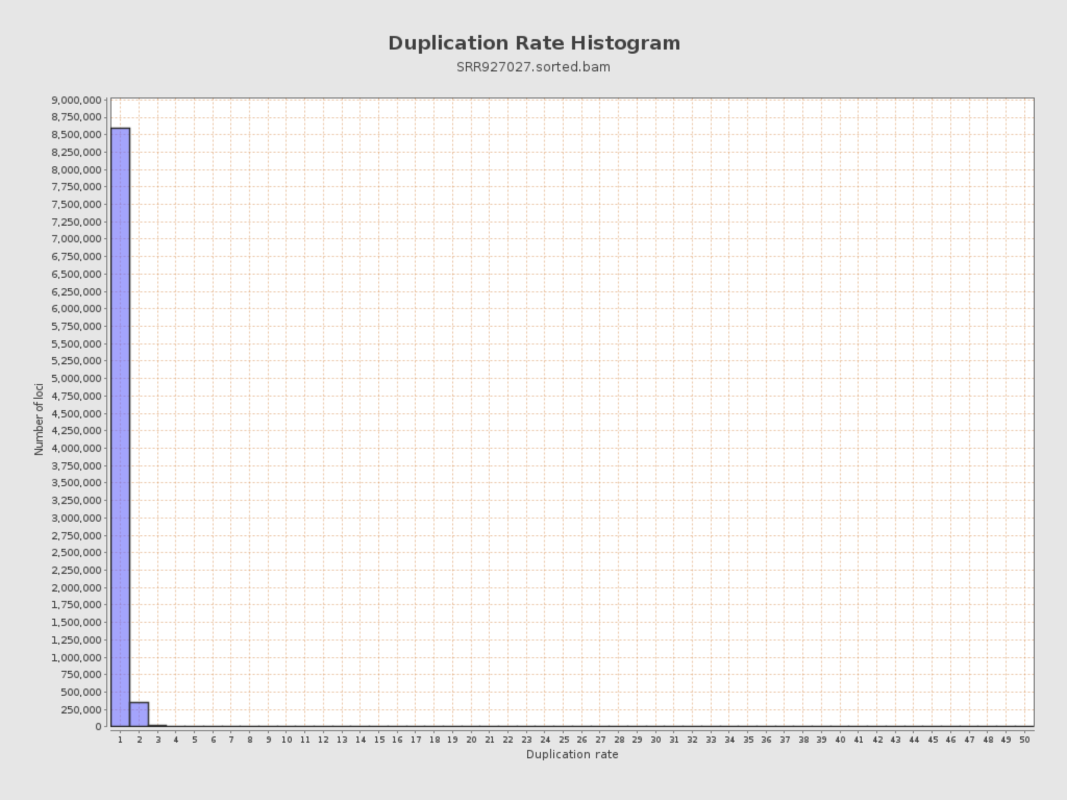
5. Results : Coverage Histogram (0-50X)



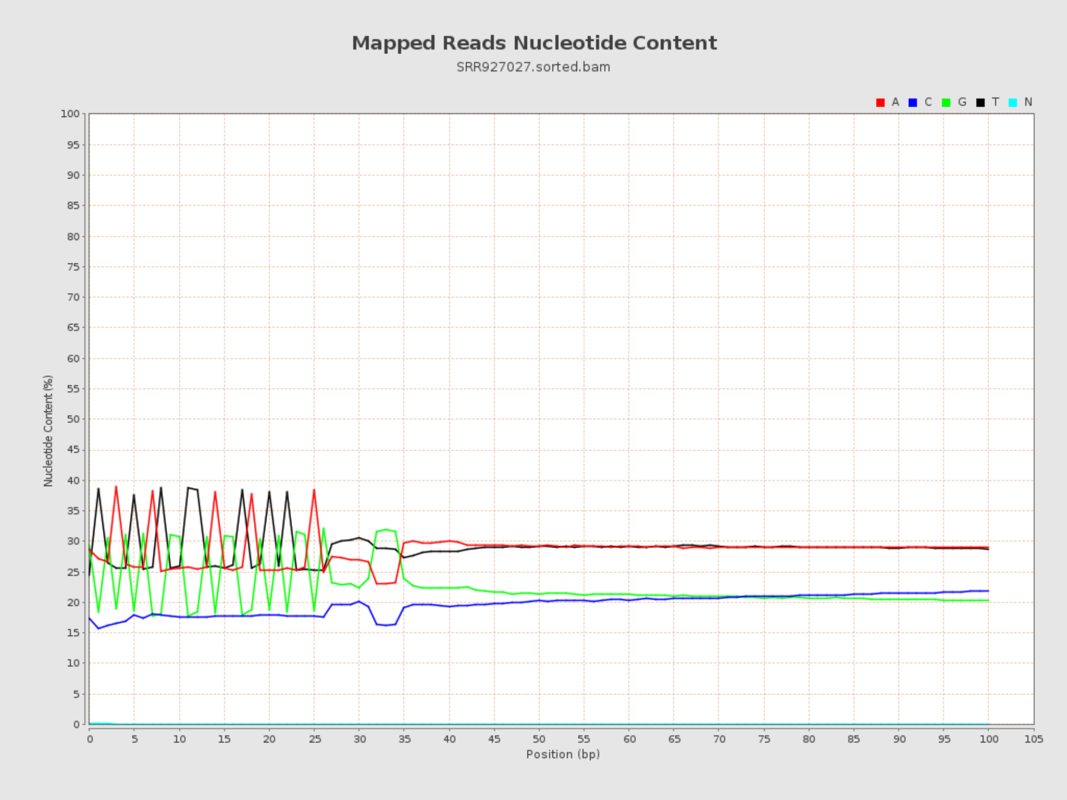
6. Results : Genome Fraction Coverage



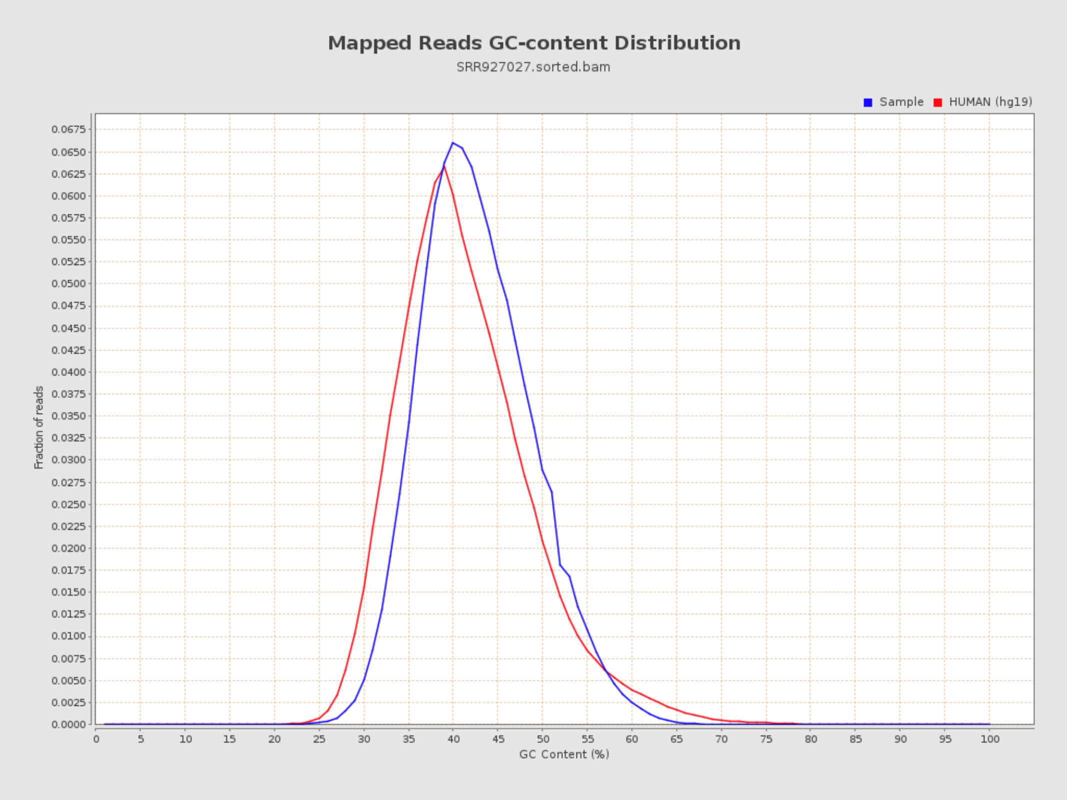
7. Results : Duplication Rate Histogram



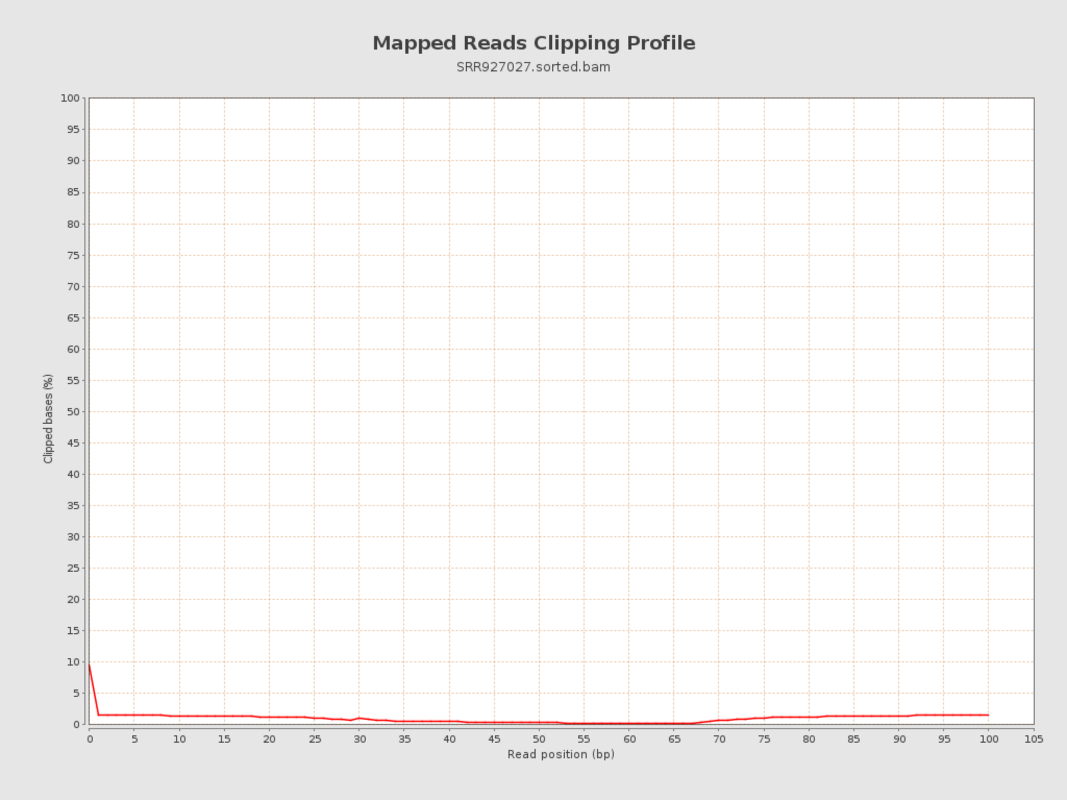
8. Results : Mapped Reads Nucleotide Content



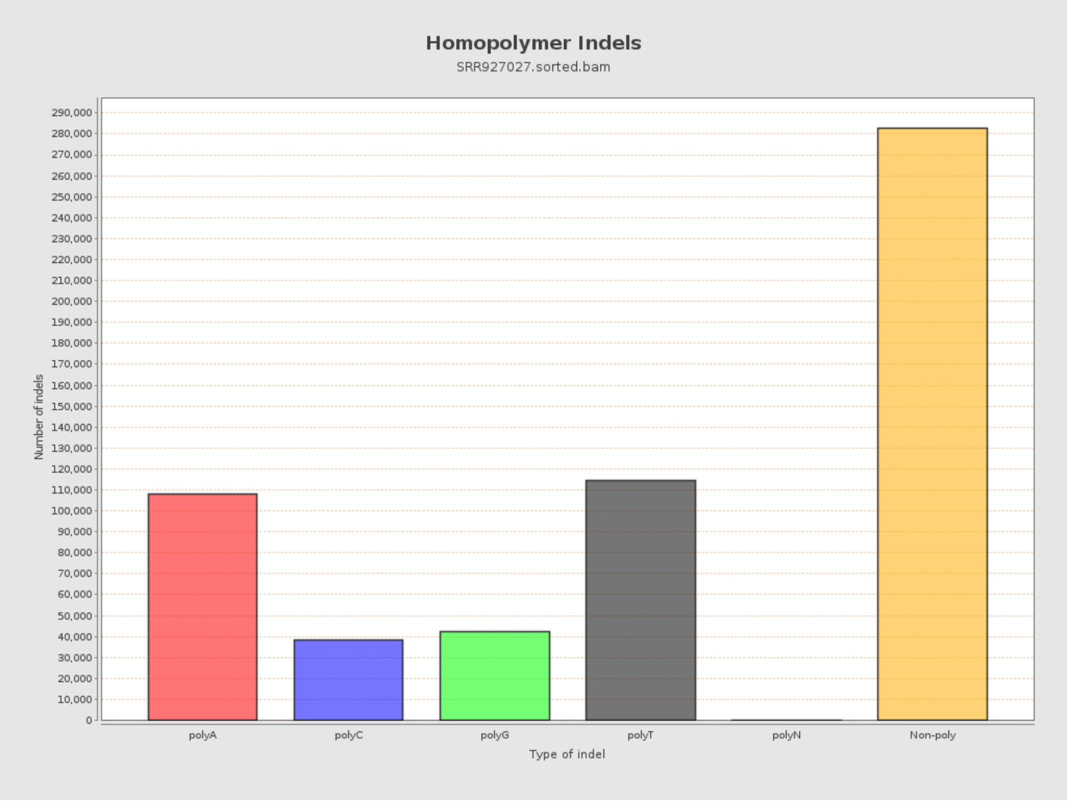
9. Results : Mapped Reads GC-content Distribution



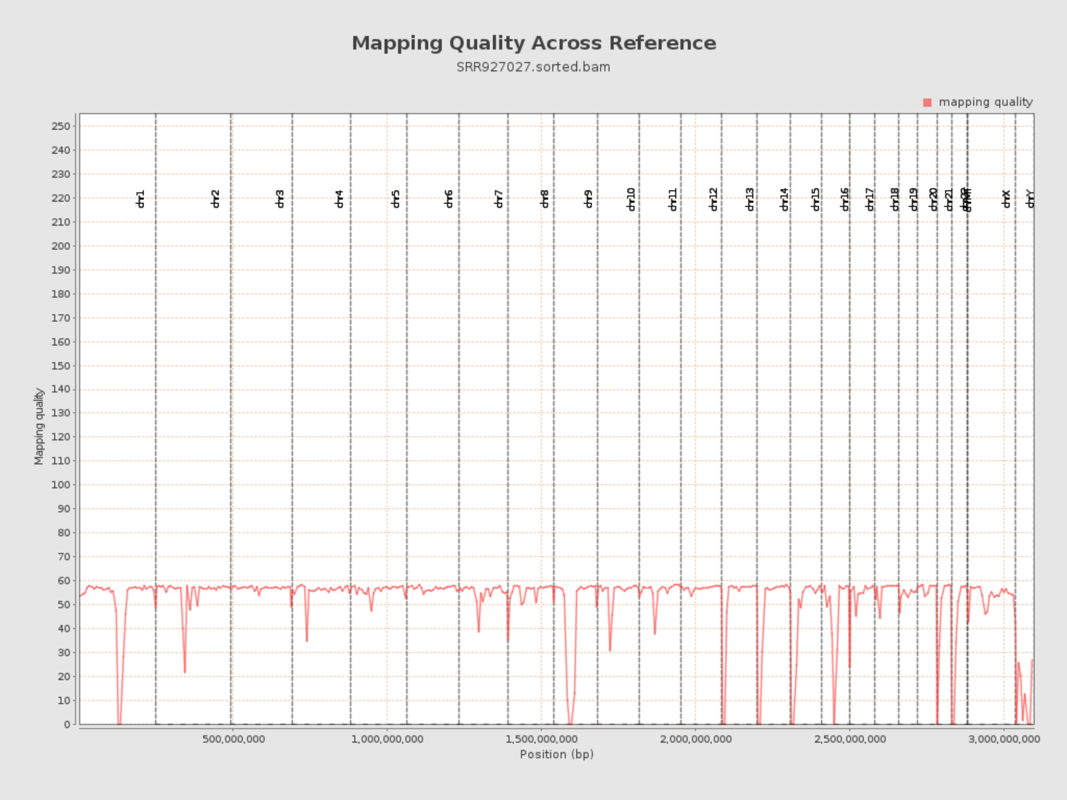
10. Results : Mapped Reads Clipping Profile



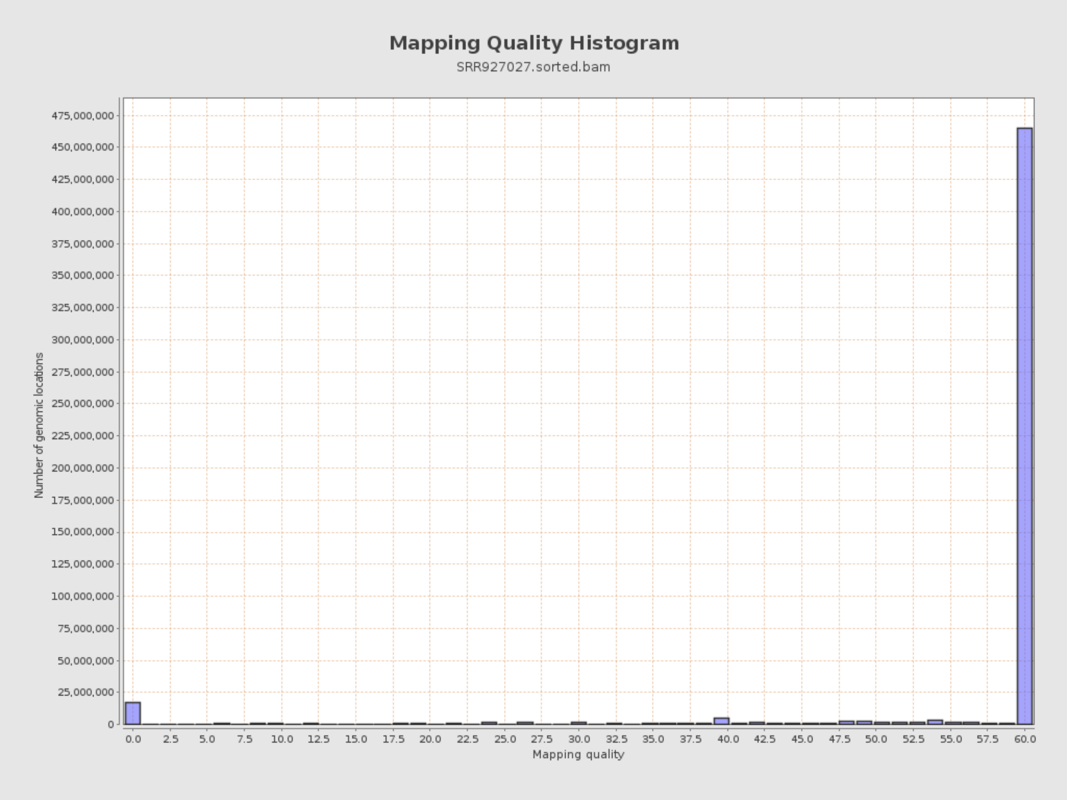
11. Results : Homopolymer Indels



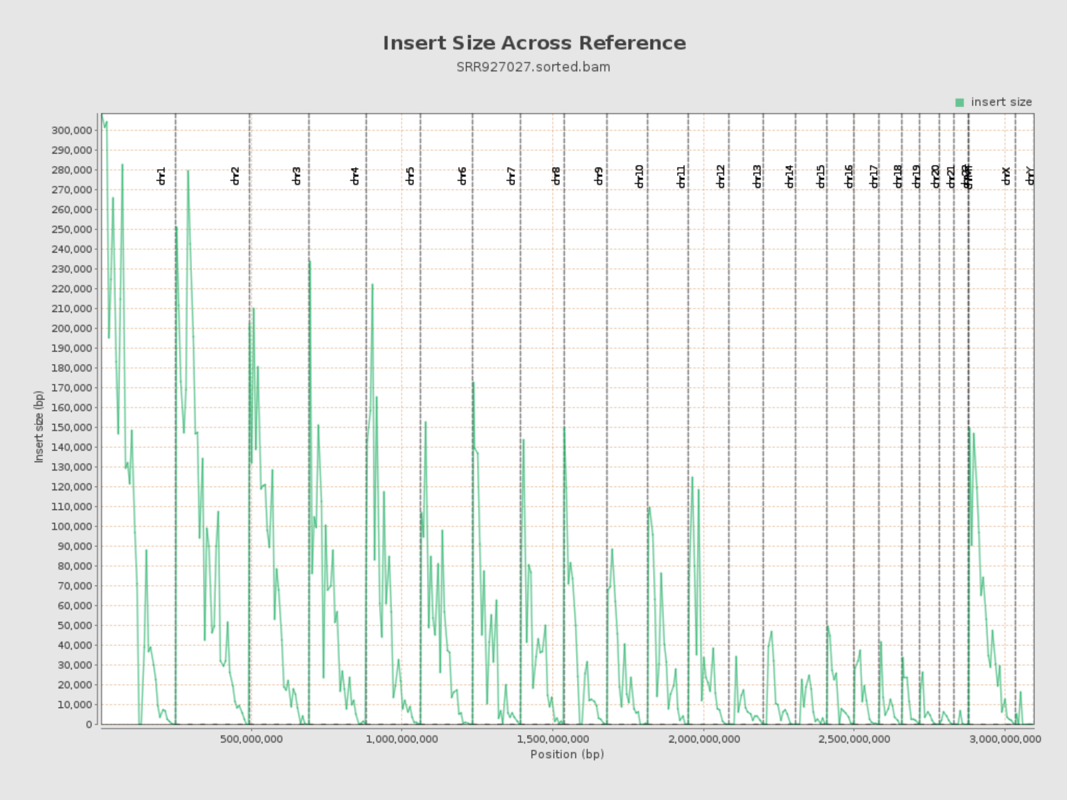
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram